

TRANSFERABILITY OF A PREDICTIVE *ROBINIA PSEUDACACIA* DISTRIBUTION MODEL IN NORTHEAST SLOVENIA

PRENOSLJIVOST NAPOVEDNEGA MODELA RAZŠIRJENOSTI VRSTE *ROBINIA PSEUDACACIA* V SEVEROVZHODNI SLOVENIJI

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Robinia pseudacacia in the Prekmurje region.
Robinija v Prekmurju.

Transferability of a predictive *Robinia pseudacacia* distribution model in northeast Slovenia

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ABSTRACT: The main goal of this study is to assess the transferability of a species distribution model (SDM) for *Robinia pseudacacia* (black locust) to two testing sites in the Prekmurje region in northeast Slovenia. The predictive performance of the SDM at the testing sites was measured by 1) visual evaluation, 2) confusion matrix, 3) true positive rate (TPR), 4) the maximum of the true skill statistics (TSS) over possible cutoffs, and 5) paired-sample ANOVA. We show that the model adequately predicted potential distribution of the species in the region, which ensures that extension of the prediction at this scale will be a reliable base for nature conservation decisions. This also serves as a positive example for within-region transfer and extension of SDMs.

KEY WORDS: geography, invasive species, landscape features, species distribution model, transferability, Prekmurje

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1 Introduction

Slovenia is among the European countries with best-preserved nature and the highest biological and landscape diversity (Ciglič 2009; Ciglič and Perko 2013; Ciglič and Oštir 2014). This is reflected by the size of Slovenian territory that is protected: 52% of the country lies within ecologically important areas and approximately 35% within Natura 2000 sites (Žvikart 2010). However, Slovenia is also subject to many pressures, one of them being biological invasions. Over the past decade, the cover of invasive species has been increasing. So far, thirty to sixty plant species in Slovenia are considered invasive (Jogan 2000), and *Robinia pseudacacia* (black locust) is one of the species with the potentially greatest negative influence on the biodiversity of natural habitats in Slovenia (Zelnik 2012).

Biological invasions are considered to be the second greatest reason for the loss of biodiversity worldwide (Vitousek et al. 1996). The effects of invasive species on areas invaded are manifold. These species may alter the disturbance regime of the sites they invade (D'Antonio and Vitousek 1992; Hejda and Pyšek 2006), competitively exclude native species and decrease native biodiversity (Walker and Vitousek 1991), alter ecosystem structure (Vitousek et al. 1996; Higgins et al. 1999; D'Antonio and Mack 2001), and lead to enormous economic costs, including decreases in timber growth rates and forest values when forest ecosystems are invaded (Pimentel 2005; Gurevitch et al. 2006). Some ecologists also believe that plant invasions contribute substantially to plant species extinctions (Mooney and Drake 1989; Vitousek 1994; Wilcove et al. 1998). Rodríguez-Labajos et al. (2009) summarized the major socioeconomic driving forces of biological invasions as 1) anthropogenic activities, 2) policies/policy level, and 3) ideology/lifestyle.

Due to their socioeconomic (Pimentel et al. 2001) and environmental effects, biological invasions have increasingly been recognized as a great problem worldwide (Ribeiro et al. 2011). The development of effective strategies to manage and monitor the spatial distribution of invasive species requires data on the habitat preferences of these species and knowledge of how landscape features influence their spatial distribution and establishment. However, detailed data collection is time consuming and logistically demanding (Preuss et al. 2011). Therefore efforts have been made to map invasive species spread in the landscape and to model and predict its spatial distribution into unknown areas (e.g., Liu et al. 2005; Vanderhoof et al. 2009; Ribeiro et al. 2011). Maps of predictive species distributions often rely on statistical models relating observations of species to environmental predictors, and projecting the fitted relationship into geographic space to produce distribution maps (Maggini et al. 2006; Randin et al. 2006; Fukasawa et al. 2009; Sundblad et al. 2009; Guisan et al. 2013; Verbruggen et al. 2013). These distribution maps are becoming a useful tool when dealing with restrictive field data and large spatial and temporal terms (Guisan and Thuiller 2005) and are also a valuable tool for environmental management and conservation (Razpotnik 2007; Barbosa et al. 2009; Sundblad et al. 2009). Despite the recent increase in species distribution models (SDM) in the literature, evidence of the practical utility of these models in real-world conservation management (Guisan et al. 2013), and aspects such as the importance of validation of these models and their transferability to other areas have not been intensively studied (Randin et al. 2006; Sundblad et al. 2009). Guisan et al. (2013) found various examples of the practical use of SDMs to guide decisions in various conservation fields, such as 1) managing biological invasions, 2) identifying and protecting critical habitats, 3) regional conservation planning, and 4) informing the translocation of threatened or captive-bred populations. The use of SDMs for conservation purposes is limited by the availability of suitable data, skilled staff, and modelling tools (Guisan et al. 2013). Its utility for applications in biological invasions by predicting areas of potential occupancy in order to target its control also depends on their transferability between regions (Verbruggen et al. 2013). Transferability of the models refers to the case when a model is applied to an area outside the site it was trained on. Preferably the range of the predictor variables (environmental variables) should be the same, or wider, at the training site than at the sites the model is applied to (Peterson et al. 2007; Sundblad et al. 2009).

The main goal of this study is to examine the transferability of an existing SDM of *R. pseudacacia* (by Ribeiro et al. 2011) to two testing areas within the same region. To model the potential distribution of *R. pseudacacia*, we used a generalized linear model (GLM) in which the presence/absence of *R. pseudacacia* was used as dependent variable and environmental variables as predictors. The results of the model indicated the most important environmental factors for species occurrence: land use, soil type, distance to the road network, and distance to water bodies. The major part of the distribution pattern observed was explained by land use, with meadows and pastures most prone to invasion by *R. pseudacacia*. The distance from water bodies has a negative influence on the species occurrence, according to the model. The distance to the road

network influences *R. pseudacacia* distribution in a non-linear way; closer to roads the probability of finding the species is higher, and this probability decreases when roads are within a distance between 100 and 300 m, while a distance longer than 300 m increases the probability of *R. pseudacacia* occurrence again. Regarding the predictor soil type, fluvisols are significantly less susceptible to *R. pseudacacia* than cambisols, and they also differ in this manner from urban soils.

2 Methods

2.1 Study area

This research was conducted in the northeastern part of Slovenia, in the Prekmurje region. Although agriculture still prevails in this region (Gabrovec and Kladnik 1997; Cunder 2009), around 29% of the landscape is forested, resulting in a high level of fragmentation (Hladnik 2005). According to its topographical features, Prekmurje can be divided into three geographical areas, which are ecologically dissimilar as well; the northern hilly area of Goričko, the central floodplains of the Mura River, known as Ravensko, and the southern lowlands known as Dolinsko (Čarni et al. 2008).

The Mura floodplains, due to their high biological diversity, host habitats of greatest importance for nature protection and are therefore included in the Natura 2000 network (Globevnik and Mikoš 2009; Košir et al. 2013). Sixty-five percent of the floodplains are forested, and ten percent is covered by *R. pseudacacia* (Globevnik and Kaligarič 2005). Along the Mura River well-drained and nutrient-rich soils prevail (Košir et al. 2013), which are most suitable for agriculture (Perko and Orožen Adamič 1998); therefore intensive agriculture is present here (Vovk Korže 2002).

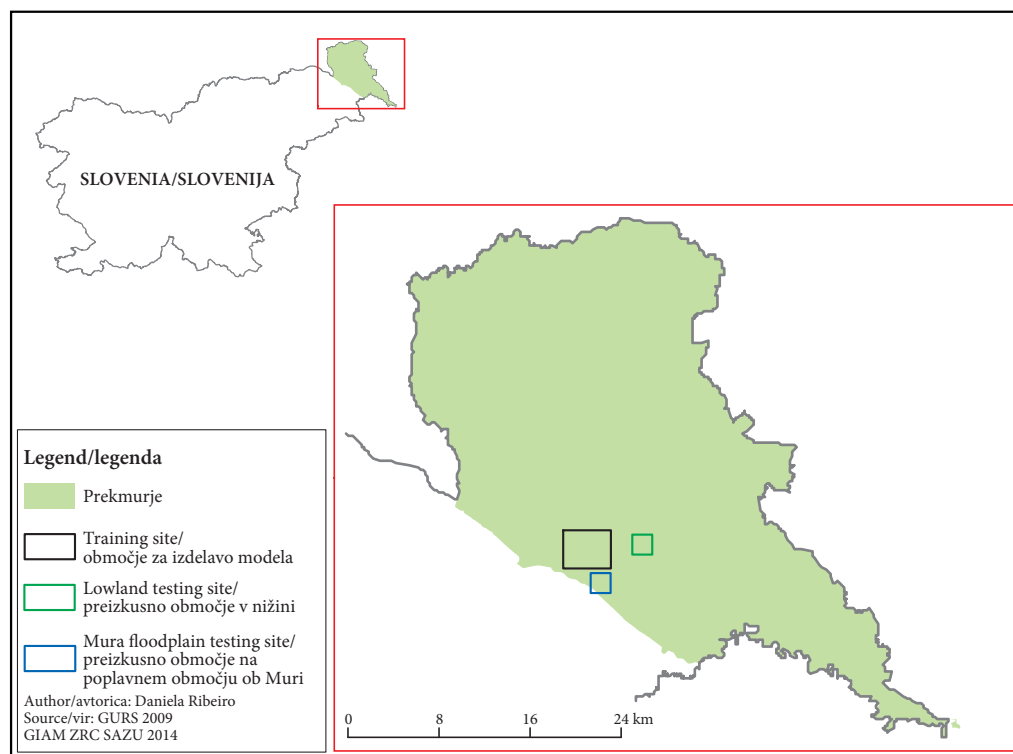


Figure 1: Location of the study area, showing the training and testing sites.

The central part of the lowlands of Prekmurje is occupied by gravelly fields safe from floods; therefore it is densely populated and intensively cultivated. The northern and southern parts are wetter and less populated (Perko and Orožen Adamič 1998). *R. pseudacacia* aggressively regenerates in the lowland area, mainly due to the decrease in groundwater level and openings in stands of forest, which creates ideal conditions for its development (Rudolf and Brus 2006).

In the southern lowland part of the study region, a training site of 12 km² was chosen to build the SDM and two testing sites were selected to assess the accuracy and transferability of the *R. pseudacacia* distribution model, one in the lowland and one in the Mura floodplains (see Figure 1). The testing sites measured 4 km² and were demarcated outside the area used to build the model (i.e., the training site; for more information, see Ribeiro et al. 2011).

2.2 Data

This study focuses on the introduced and highly invasive species *R. pseudacacia* L. This species was selected due to its abundance in the study region (Wraber 1951; Rudolf and Brus 2006; Kutnar and Kobler 2013; Kutnar and Pisek 2013) and its presence in the country for over a century (Novice 1858). For both testing sites, *R. pseudacacia* occurrence was determined from the visual interpretation of spring orthophotos. Somodi et al. (2012) have shown that orthophotos taken during the flowering period of *R. pseudacacia* provide the best sources for its recognition and thus a potential basis for monitoring. All patches with the species' presence, independent of its size, were digitized in a geographic information system environment.

For application of the model, a grid 10 m wide was generated by regular point generation at the testing sites. We resampled the set of predictor variables shown by Ribeiro et al. (2011) to be relevant for *R. pseudacacia* to these grids of both testing sites, using ArcGIS 9.3. The source of variables that contributed to the model included the following: land use (Zemljiški kataster 2009), soil type (Pedološka karta Slovenije 2007), distance to the road network, and distance to water bodies (Državna topografska karta 2009).

2.3 Predictions and evaluation

The SDM for *R. pseudacacia* built by Ribeiro et al. (2011) using a GLM was applied to the testing sites, enabling assessment of the generality of habitat preferences deduced at the training site and a test of its transferability. The predictive ability of the SDM was tested at the testing sites and contrasted with its performance at the training site.

The predictive performance of the SDM at the testing sites was measured by: 1) visual evaluation, looking at spatial predictions and observed presences of the species, 2) confusion matrices, 3) true positive rate, also called sensitivity (Fielding and Bell 1997), 4) the maximum of the true skill statistics (Allouche et al. 2006) over possible cutoffs, and 5) paired-sample ANOVA. Distributions of TPR at the specific testing sites were compared in an ANOVA-like setting, in which the values of the index at the same cut were treated as paired samples (for details, see Somodi et al. 2012). Tukey contrasts were also applied, which make the procedure equivalent to a Tukey post-test. The confusion matrix records the frequencies of each of the four possible types of outcome of prediction success: 1) true positives, 2) false positives, 3) false negatives, and 4) true negatives. True positives is the number of occurrences in which the presence of the species was correctly identified, false positives is the number of positive predictions in which no presence was observed, false negatives is the number of presences in which the model did not predict occurrences (Fielding and Bell 1997; Somodi et al. 2012), and true negatives is the number of absences that were correctly predicted by the model. False negatives do not only reflect our errors, but also arise because the species is not yet present (and our estimation falls at a point still negative), though the site may be suitable for the species. This is a common problem in habitat suitability modelling, which makes AUC and ROC curves potentially misleading (Lobo et al. 2008). Therefore, we relied on the ratio between true positive cases and all positive cases, in which the presence of the species was correctly identified by the model (TPR). In addition, the maximum of TSS was introduced to replace the traditional maximum Kappa measure because it is free of prevalence bias (Allouche et al. 2006) and was used to cut the probability distribution into a presence/absence binary map.

Finally, the comparison of the TPR curves, emerging from values calculated at regular cuts along the probability gradient from the training and testing sites, was done using a method conceptually corresponding to paired-sample ANOVA. The appropriate way to perform such a test is to use linear mixed models, with site identity as a random variable and the predictor variables as fixed effects (the function used in R was »lme«, »nlme« package; Pinheiro et al. 2014). A Tukey post test was also applied to the mixed model to assess pairwise significance in order to determine which sites differed significantly from one another (for details, see Somodi et al. 2012).

The application of the SDM to the testing sites and the evaluation of its accuracy and transferability were implemented in the R Statistical environment (R Core Development Team 2008). The SDM was exported from the R Statistical environment as tables describing each predictive probability point-by-point and projected in ArcGIS 9.3.

3 Results

The prediction of the SDM for *R. pseudacacia* was first verified by spatial overlapping at the existing locations with predicted values of probability occurrence. There was a good degree of overlap between predicted and observed *R. pseudacacia* at the testing sites (Figures 2 and 3).

The probability of occurrence was assigned to each sampling point. Map colours were selected to reflect major breakpoints at TPR curves (Figure 4). Two major breakpoints (at 0.5 and 0.3) are apparent for the lowland site, and therefore the highest probability classes were defined as 0.5–1 (red) and 0.3–0.5 (orange). Lower probabilities were separated into three equal classes in ascending order: 0.00–0.08 (dark green), 0.08–0.15 (light green), and 0.15–0.30 (yellow).

The predicted distribution for the testing sites beyond the known occurrences of the species indicates that those sites are suitable for invasion.

The prediction resulting from the SDM was a good match with the observed presence of the species at both testing sites (Figures 2 and 3). Substantial observations fall into the predicted category with a higher probability than 0.50. Some of the observed areas that were outside this probability were included in the next category (0.30–0.50) and a few in the remaining categories.

Table 1: Confusion matrix for the Lowland testing site at the probability cut corresponding to the maximum TSS. Predicted presence/absence [1/0] of *R. pseudacacia* crosstabulated with observations.

		Observed <i>R. pseudacacia</i>	
		0	1
Predicted <i>R. pseudacacia</i>	0	25128	434
	1	4201	1368

Table 2: Confusion matrix for the Mura floodplain testing site at the probability cut corresponding to the maximum TSS. Predicted presence/absence [1/0] of *R. pseudacacia* crosstabulated with observations.

		Observed <i>R. pseudacacia</i>	
		0	1
Predicted <i>R. pseudacacia</i>	0	14301	230
	1	12160	2330

The results from the confusion matrices indicate that the majority of presences predicted fell into the presences observed (Tables 1 and 2). Nevertheless, as can be seen, these tables present better results for the Mura floodplain than for the Lowland testing site.

The TPR and TSS values at specific probability cuts at the Mura floodplain and Lowland testing sites can be seen in Figures 4 and 5, respectively.

Table 3: Comparison of TPR curves by paired-sample ANOVA with Tukey post test.

	Estimate	Std. Error	z value	Significance
Mura: Lowland = 0	0.007	0.003	2.353	$p < 0.1$
Training: Lowland = 0	-0.011	0.003	-3.408	$p < 0.01$
Training: Mura = 0	-0.018	0.003	-5.761	$p < 0.001$

The comparison between the predictions for the training site and the testing sites shows a significant difference, meaning that the testing sites were predicted worse than the training site (Table 3).

The SDM from the training site was successfully used to generate maps of potential distributions at the testing sites. However, as expected, the SDM achieves better predictive results at the training site than at the testing sites.

4 Discussion

We were able to successfully transfer the SDM for *R. pseudacacia* built by Ribeiro et al. (2011) to two testing sites within the same geographical region. A GLM was a reliable method to model the range of potential habitats for the species to new sites; this result is consistent with Randin et al. (2006), who argued that a GLM is a robust modelling method for transferability. However, Araújo et al. (2005) found that a generalized additive model showed better transferability than a GLM.

Generally the SDM adequately predicted the potential distribution of *R. pseudacacia* in the Prekmurje region; however, significant differences appeared regarding its success at the two testing sites. It can at least be inferred that our model performs adequately for a slightly different geographical setting, albeit within one region.

Most studies testing models outside the training area use one testing site only (e.g., Randin et al. 2006; Fukasawa et al. 2009; Sundblad et al. 2009; Preuss et al. 2011) and there are only a few examples using more than one testing site (Zimmermann and Kienast 1999; Wenger and Olden 2012). Our study is also valuable as a contribution to the latter group. Nevertheless its generalizability to other geographic regions may be limited and the extrapolation of its results should be treated with prudence; this should be done with careful examination of the underlying environmental predictors. One of the most important conditions for the practical use of SDMs to guide environmental management decisions is their transferability within and among other regions. As shown by Barbosa et al. (2009), SDMs are best at describing the spatial pattern of species at the site the model was trained in, mainly because different localities may have differences in the ranges of environmental predictors (Randin et al. 2006). Environmental differences between different geographical regions may therefore limit the usefulness of this type of model, and such models may yield unrealistic predictions outside the domain used to build the models (Barbosa et al. 2009). Thus the availability of data can be a limiting factor in the spatial transfer of SDMs. In addition to this limitation, the choices made during the modelling process, such as the modelling technique selected, affect its transferability to other areas, as shown by Araújo et al. (2005) and Randin et al. (2006). It was beyond the scope of our study to assess the robustness of modelling techniques when transferred from one geographical region to another, but we did transfer the model within the same geographical region.

The greatest value of our study is that the predictions of the likelihood of occurrence of the species at non-surveyed sites may warn managers of the potential threat of planting or spontaneous spread, which may support conservation planning. We have shown that the predictive model tested here can reliably be applied for region-wide predictions, which helps raising awareness among the public about this invasive species. This is vital for combating further spread, especially in the study region, where locals predominantly perceive the benefits of the species. The application of a model already constructed for predicting the possible extent of range expansion of *R. pseudacacia* offers an easy tool for managers to mitigate the impact of this invasive species and is an alternative to time-consuming and logistically demanding data collection.



Figure 2: Potential habitat map of *R. pseudacacia* for the lowland testing site.



Figure 3: Potential habitat map of *R. pseudacacia* for the Mura floodplain testing site.

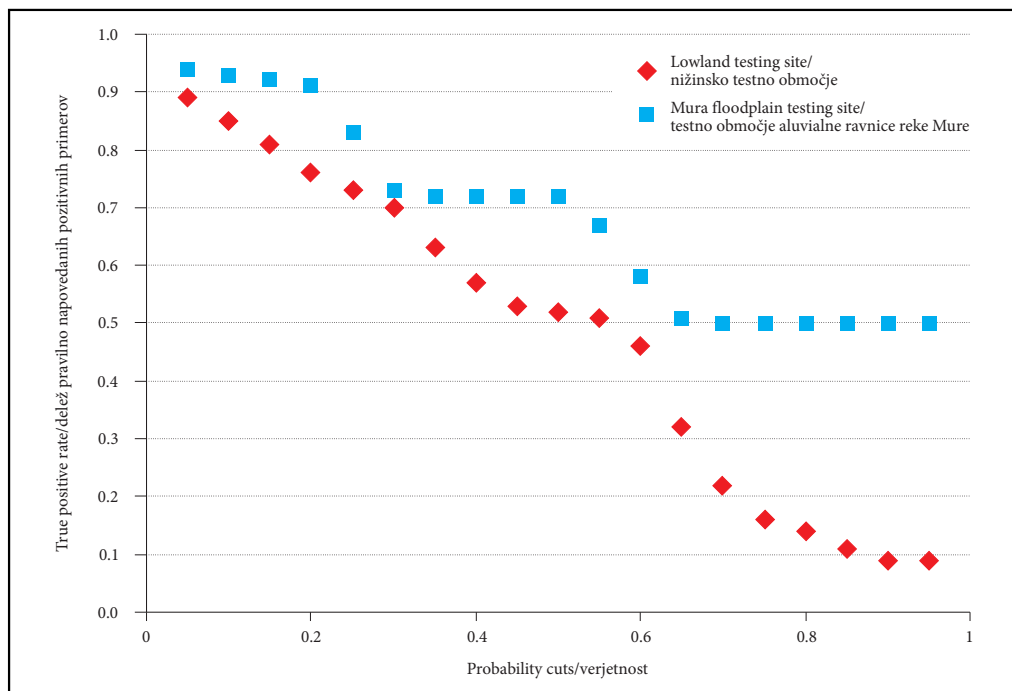


Figure 4: True positive rate measurement of predictive accuracy for the testing sites.

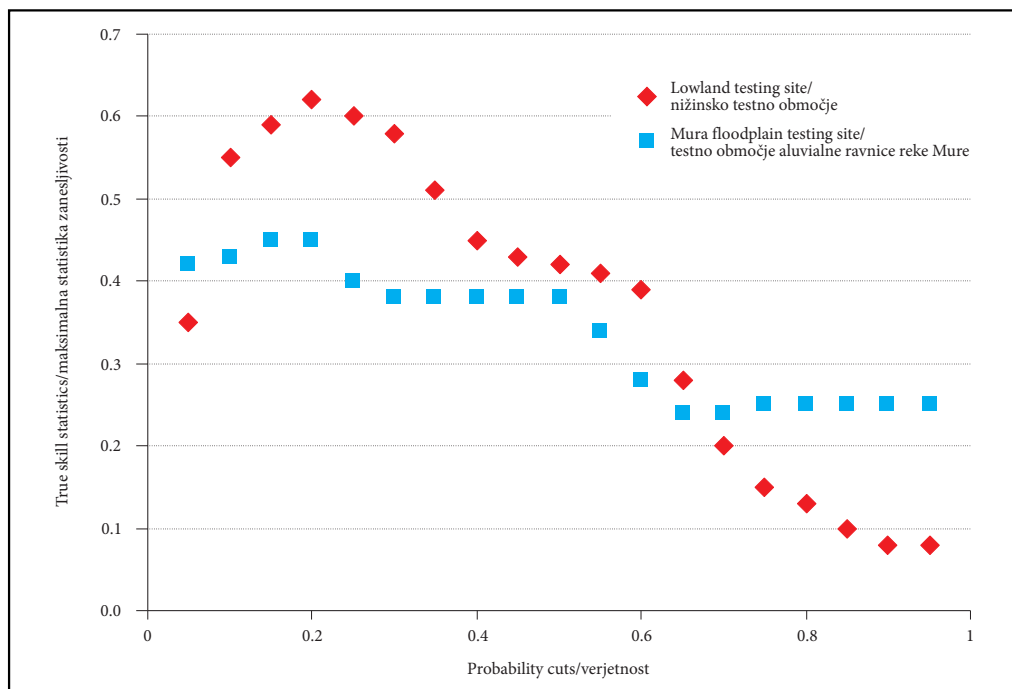


Figure 5: True skill statistics measurement of predictive accuracy for the testing sites.

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Prenosljivost napovednega modela razširjenosti vrste *Robinia pseudacacia* v severovzhodni Sloveniji

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IZVLEČEK: Glavni namen raziskave je oceniti prenosljivost napovednega modela razširjenosti vrste (NMRV) *Robinia pseudacacia* na dve testni območji v Prekmurju v severovzhodni Sloveniji. Napovedno uspešnost NMRV na testnih območjih smo merili z 1) vizualnim ocenjevanjem, 2) matriko razvrstitev, 3) deležem pravilno napovedanih pozitivnih primerov, 4) maksimalno statistiko zanesljivosti (ang. *True Skill Statistics* ali TSS) in 5) analizo variance odvisnih vzorcev. Raziskava kaže, da je model ustrezno napovedal potencialno razširjenost vrste na tem območju, kar pomeni, da bo na podlagi napovedi za celotno regijo mogoče sprejemati zanesljive odločitve na področju ohranjanja narave. Poleg tega gre pri tem za pozitivni primer prenosa in razširitve NMRV znotraj iste regije.

KLJUČNE BESEDE: geografija, invazivne vrste, pokrajinske značilnosti, model razširjenosti vrste, prenosljivost, Prekmurje

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1 Uvod

Slovenija spada med evropske države z najbolje ohranjeno naravo in najvišjo stopnjo biološke in pokrajinske pestrosti (Ciglič 2009; Ciglič in Perko 2013; Ciglič in Oštrir 2014). To je vidno tudi v površini zavarovanega slovenskega ozemlja: 52 % dežele leži na ekološko pomembnih območjih in približno 35 % njene površine pokrivajo območja Nature 2000 (Žvikart 2010). Slovenija pa je podvržena tudi mnogim obremenitvam, med drugim tudi biološkim invazijam. V zadnjem desetletju se pokritost z invazivnimi rastlinskimi vrstami povečuje. Doslej so v Sloveniji potrdili trideset do šestdeset invazivnih rastlinskih vrst (Jogan 2000), robinija (*Robinia pseudacacia*) pa je ena izmed vrst s potencialno največjim negativnim vplivom na biotsko raznovrstnost slovenskih naravnih habitatov (Zelnik 2012).

Biološke invazije v svetu veljajo za drugi najpomembnejši razlog za izgubo biotske raznovrstnosti (Vitousek s sod. 1996). Invazivne vrste imajo za območja, na katera se razširijo, raznolike posledice. Spremenijo lahko režim motenj na območjih, kamor se razširijo (D'Antonio in Vitousek 1992; Hejda in Pyšek 2006), izrinejo avtohtone vrste in zmanjšajo avtohtono biotsko raznovrstnost (Walker in Vitousek 1991), spremenijo strukturo ekosistema (Vitousek s sod. 1996; Higgins s sod. 1999; D'Antonio in Mack 2001) in povzročijo ogromne ekonomske stroške, vključno z zmanjšanjem prirastka lesa in vrednosti gozda v primeru širjenja v gozdne ekosisteme (Pimentel 2005; Gurevitch s sod. 2006). Nekateri ekologi menijo, da invazivne rastlinske vrste pomembno prispevajo k izginjevanju rastlinskih vrst (Mooney in Drake 1989; Vitousek 1994; Wilcove s sod. 1998). Rodríguez-Labajos s sodelavci (2009) so glavne družbenoekonomske gonilne sile bioloških invazij razdelili v tri skupine: 1) antropogeni dejavniki, 2) politična raven in 3) nazor/živiljenjski slog.

Zaradi svojih družbenoekonomskih (Pimentel s sod. 2001) in okoljskih posledic biološke invazije postajajo vse večji problem na svetovni ravni (Ribeiro s sod. 2011). Za oblikovanje učinkovitih strategij upravljanja in spremljanja prostorske razširjenosti invazivnih vrst potrebujemo podatke o tem, v katere habitate se te vrste raje naseljujejo, poleg tega pa moramo vedeti tudi, kako pokrajinske značilnosti vplivajo na prostorsko razširjenost in uveljavitev teh vrst. Zbiranje podrobnih podatkov pa je dolgotrajno in logistično izredno zahtevno (Preuss s sod. 2011), zato poskušajo raziskovalci izdelati karte razširjenosti invazivnih vrst v pokrajini ter modelirati in napovedati njihovo širjenje na druga območja (npr. Liu s sod. 2005; Vanderhoof s sod. 2009; Ribeiro s sod. 2011). Napovedne karte razširjenosti vrst pogosto temeljijo na statističnih modelih, ki prisotnost vrst povezujejo z okoljskimi napovednimi dejavniki (prediktorji) ter izračunano razmerje projicirajo v geografski prostor in tako oblikujejo karte razširjenosti (Maggini s sod. 2006; Randin s sod. 2006; Fukasawa s sod. 2009; Sundblad s sod. 2009; Guisan s sod. 2013; Verbruggen s sod. 2013). Te karte postajajo uporabno orodje v primerih, ko imamo opravka z omejenimi terenskimi podatki ter obsežnimi prostorskimi in časovnimi zahtevami (Guisan in Thuiller 2005). Poleg tega so dragoceno orodje na področju upravljanja in ohranjanja okolja (Razpotnik 2007; Barbosa s sod. 2009; Sundblad s sod. 2009). Kljub temu da je v literaturi v zadnjem času viden porast obravnave modelov razširjenosti vrst (NMRV) in primeri njihove praktične uporabe pri dejanskem ohranjanju narave še niso bili preučeni v zadostni meri (Guisan s sod. 2013). Prav tako niso bili raziskani različni drugi vidiki, kot sta pomen validacije teh modelov in njihova prenosljivost na druga območja (Randin s sod. 2006; Sundblad s sod. 2009). Guisan s sod. (2013) so našli različne primere praktične uporabe NMRV, ki lahko usmerjajo odločitve na različnih področjih ohranjanja, kot so 1) upravljanje bioloških invazij, 2) določanje in varovanje ogroženih habitatov, 3) regionalno načrtovanje programov zaščite in 4) prenos ogroženih populacij ali populacij, gojenih v ujetništvu. Uporabo NMRV za namene ohranjanja vrst omejuje razpoložljivost ustreznih podatkov, ustrezno usposobljenega osebja in orodij za modeliranje (Guisan s sod. 2013). Pri obravnavi bioloških invazij lahko te modele uporabimo za napovedovanje območij morebitne prisotnosti invazivnih vrst za namene nadzorovanja njihove širitve, vendar je uporabnost modelov v tem pogledu odvisna tudi od njihove prenosljivosti med regijami (Verbruggen s sod. 2013). O prenosljivosti govorimo, ko model uporabimo zunaj območja, na katerem smo ga prvotno razvili (t. i. učnega območja). Če je le mogoče, mora biti razpon napovedne (okoljske) spremenljivke na učnem območju enake ali širše kot na območjih, na katera je model prenesen (Peterson s sod. 2007; Sundblad s sod. 2009).

Glavni cilj te raziskave je preučiti prenosljivost obstoječega modela razširjenosti robinije (*Robinia pseudacacia*) (Ribeiro s sod. 2011) na dve testni območji v isti regiji. Za modeliranje potencialne razširjenosti robinije smo uporabili generalizirani linearni model (GLM), pri katerem smo za odvisno spremenljivko uporabili prisotnost/odsotnost robinije, napovedne dejavnike pa smo uporabili kot okoljske spremenljivke. Model je pokazal najpomembnejše okoljske dejavnike, ki vplivajo na pojavnost vrst: raba tal, vrsta prsti,

oddaljenost od cestnega omrežja in oddaljenost od vodotokov. Na vzorec razširjenosti najbolj vpliva raba tal, pri čemer so invazijam robinije bolj izpostavljeni travniki in pašniki. Oddaljenost od vodotokov negativno vpliva na pojavnost vrste, oddaljenost od cestnega omrežja pa na razširjenost vrste vpliva nelinearno. V bližini cest je verjetnost, da bomo našli robinijo, večja, pri čemer se na oddaljenosti 100–300 m od ceste ta verjetnost zniža, na oddaljenosti več kot 300 m pa se spet poveča. Z vidika prsti robinja veliko bolje uspeva na rjavih prsteh (kambisolih) kot na obrečnih prsteh (fluvisolih), ki se v tem pogledu tudi razlikujejo od prsti oziroma tal na urbanih površinah.

2 Metode

2.1 Območje raziskave

Raziskava je potekala v Prekmurju na severovzhodu Slovenije. Čeprav v tej regiji še vedno prevladuje kmetijstvo (Gabrovec in Kladnik 1997; Cunder 2009), je okrog 29 % pokrajine prekrte z gozdom, zaradi česar je za to območje značilna visoka stopnja razdrobljenosti pokrajine (Hladnik 2005). Z vidika topografskih značilnosti lahko Prekmurje razdelimo v tri ekološko različna geografska območja: severno hribovito območje Goriškega, osrednjo aluvialno ravnico reke Mure, poznano pod imenom Ravensko, in južno nižavje, poznano pod imenom Dolinsko (Čarni s sod. 2008).

Zaradi visoke stopnje biotske raznovrstnosti so habitati na aluvialnih ravninah reke Mure izredno pomembna naravovarstvena območja, ki so vključena v mrežo Natura 2000 (Globevnik in Mikoš 2009; Košir s sod. 2013). 65 % aluvialnih ravnin prekriva gozd, 10 % pa jih prerašča robinija (Globevnik in Kaligarič 2005). Vzdolž Mure prevladujejo rodovitna tla, ki dobro prepuščajo vodo (Košir s sod. 2013) in so najprimernejša za kmetijstvo (Perko in Orožen Adamič 1998); za to območje je zato značilno intenzivno kmetijstvo (Vovk Korže 2002). Osrednji del prekmurske nižine sestavljajo prodnata polja, ki jih rečne poplave ne ogrožajo, zato so gosto poseljena in intenzivno obdelana. Severni in južni del sta bolj mokrotna in manj poseljena (Perko in Orožen Adamič 1998). Robinija se zelo agresivno pomlajuje v nižinskem svetu, kar je v veliki meri posledica vpliva nižanja podtalnice in velike presvetljenosti gozdnih sestojev, ki ustvarjata idealne pogoje za njen razvoj (Rudolf in Brus 2006).

V južnem nižinskem delu obravnavane regije smo izbrali učno območje velikosti 12 km², na katerem smo razvili NMRV, in dve testni območji, na katerih smo ocenili točnost in prenosljivost modela razširjenosti robinije, in sicer enega v nižinskem delu in enega na aluvialni ravnici reke Mure (glej sliko 1). Testni območji sta obsegali 4 km² in sta ležali izven območja, ki smo ga uporabili za oblikovanje modela (za več informacij glej Ribeiro s sod. 2011).

Slika 1: Lokacija območja raziskave z učnim območjem in dvema testnima območjema.

Glej angleški del prispevka.

2.2 Podatki

Raziskava obravnava robinijo, ki je v ta prostor prinesena in močno invazivna. Izbrali smo jo zato, ker jo lahko v preučevani regiji najdemo na velikih površinah (Wraber 1951; Rudolf in Brus 2006; Kutnar in Kobler 2013; Kutnar in Pisek 2013) in ker je v Sloveniji prisotna že več kot stoletje (Novice 1858). Prisotnost robinije na obeh testnih območjih smo določili z vizualno interpretacijo spomladanskih ortoposnetkov. Somodi s sodelavci (2012) so ugotovili, da na ortoposnetkih, narejenih v obdobju cvetenja robinije, najlažje prepoznamo in morebiti tudi spremljamo prisotnost te vrste. Vse zaplate, poraščene s to vrsto, smo digitalizirali v geografskem informacijskem sistemu ne glede na njihovo velikost.

Nato smo na testnih območjih oblikovali pravilno mrežo točk, tako da so bile posamezne celice široke 10 m. Napovedne spremenljivke, za katere je Ribeiro s sodelavci (2011) dokazala, da so primerne za obravnavo robinije, smo z uporabo ArcGIS 9.3 prenesli na mrežo na obeh testnih območjih. Spremenljivke, ki smo jih uporabili v modelu, so bile raba tal (Zemljiški kataster 2009), vrsta prsti (Pedološka karta Slovenije 2007), oddaljenost od cestnega omrežja in oddaljenost od vodotokov (Državna topografska karta 2009).

2.3 Napovedi in ocena

Na testnih območjih smo uporabili model razširjenosti vrste, ki ga je za robinijo razvila Ribeiro s sodelavci (2011) z uporabo generaliziranega linearnega modela. Na podlagi tega smo lahko ocenili, v kakšni meri lahko posplošimo ugotovitve z učnega območja glede tega, v katere habitate se vrsta raje naseljuje, in testirali prenosljivost modela. Na testnih območjih smo preverili napovedno uspešnost modela in jo primerjali z uspešnostjo na učnem območju.

Napovedno uspešnost NMRV na testnih območjih smo merili z: 1) vizualnim ocenjevanjem, tako da smo na podlagi prostorskih napovedi opazovali dejansko prisotnost vrste; 2) matrikami razvrstitev; 3) deležem pravilno napovedanih pozitivnih primerov (ang. *true positive rate* ali TPR) oziroma stopnjo občutljivosti (Fielding in Bell 1997); 4) maksimalno statistiko zanesljivosti (ang. *True Skill Statistics* ali TSS; Allouche s sod. 2006) in 5) analizo variance odvisnih vzorcev. Porazdelitvi TPR na obravnavanih testnih območjih smo primerjali v okolju, podobnim tistemu pri analizi variance (ANOVA), pri čemer smo vrednosti indeksa na istem pragu obravnavali kot odvisne vzorce (za več informacij glej Somodi s sod. 2012). Uporabili smo tudi Tukeyjevo primerjavo, zaradi česar je postopek enakovreden Tukeyjevemu *post hoc* preizkusu. Z matriko razvrstitev določimo pogostost vsake izmed štirih vrst rezultatov napovedne uspešnosti:

- pravilno napovedanih pozitivnih primerov,
- napačno napovedanih pozitivnih primerov,
- napačno napovedanih negativnih primerov in
- pravilno napovedanih negativnih primerov.

Pravilno napovedani pozitivni primeri se nanašajo na število primerov, v katerih je bila prisotnost vrste pravilno napovedana, napačno napovedani pozitivni primeri se nanašajo na število pozitivnih napovedi, pri katerih ni bilo ugotovljene prisotnosti, napačno napovedani negativni primeri na število primerov prisotnosti, pri katerih model prisotnosti ni napovedal (Fielding in Bell 1997; Somodi s sod. 2012), in pravilno napovedani negativni primeri se nanašajo na število neprisotnosti, ki jih je model pravilno napovedal. Napačno napovedani negativni primeri ne odražajo samo naših napak, saj vrsta na tem območju sploh še ni prisotna (pa tudi svojo oceno smo podali v času, ko še ni bila prisotna), a to še ne pomeni, da območje za vrsto ni primerno. To je pri modeliranju ustreznosti habitatov pogosta težava, zaradi česar sta lahko krivulji AUC in ROC zavajajoči (Lobo s sod. 2008). Zato smo se oprli na razmerje med številom pravilno napovedanih pozitivnih primerov in številom vseh pozitivnih primerov, v katerih je model pravilno ugotovil prisotnost vrste (TPR). Poleg tega smo namesto klasičnega maksimalnega koeficienta kapa raje uporabili maksimalno statistiko zanesljivosti TSS, saj ni podvržena pristranskosti zaradi (drugačne) razširjenosti (Allouche s sod. 2006); na podlagi TSS smo verjetnost razširjenosti vrste pretvorili v binarni zemljevid prisotnosti/odsotnosti.

Na koncu smo primerjali krivulje TPR, ki smo jih oblikovali na podlagi vrednosti, izračunanih v rednih presledkih vzdolž gradienta verjetnosti na učnem območju in testnih območjih; primerjali smo jih z uporabo metode, ki je po svoji zasnovi podobna analizi variance odvisnih vzorcev. Tovrstni test je najbolje izvesti z uporabo linearnih mešanih modelov, pri čemer je identiteta območja naključna spremenljivka, napovedne spremenljivke pa so stalni (fiksni) učinki (v statističnem programu R smo uporabili funkcijo »lme« v paketu »nlme«; Pinheiro s sod. 2014). Da bi ocenili statistično pomembnost v parih, smo pri mešanem modelu uporabili tudi Tukeyjev *post hoc* preizkus in tako določili območja, ki so se med seboj pomembno razlikovala (za več informacij glej Somodi s sod. 2012).

Prenos NMRV na testna območja ter oceno njegove točnosti in prenosljivosti smo izvedli v statističnem programu R (R Core Development Team 2008). Rezultate modeliranja smo iz programa R izvozili v obliki preglednic, v katerih je bila opisana napovedna verjetnost vsake točke, in rezultate projicirali v programu ArcGIS 9.3.

3 Rezultati

Rezultate NMRV za robinijo smo najprej preverili s prostorskim prekrivanjem obstoječih prisotnosti z napovedanimi prisotnostmi. Napovedana in dejanska prisotnost robinije na testnih območjih sta se v precejšnji meri ujemale (sliki 2 in 3).

Vsaki vzorčni točki smo pripisali verjetnost pojavnosti vrste. Glavne prelomne točke (točke, na katerih se pojavnost vrste poveča ali zmanjša) na krivuljah TPR smo na karti označili z različnimi barvami (slika 4). Za nižinsko območje smo ugotovili dve prelomni točki (pri vrednostih 0,5 in 0,3), na podlagi česar smo

določili razreda največje verjetnosti: 0,5–1 (označeno rdeče) in 0,3–0,5 (označeno oranžno). Nižje verjetnosti smo v naraščajočem zaporedju razdelili v tri enakovredne razrede: 0,00–0,08 (temno zeleno), 0,08–0,15 (svetlo zeleno) in 0,15–0,30 (rumeno).

Napovedana razširjenost na testnih območjih, ki je bila večja od dejanske prisotnosti vrste, kaže na to, da sta ti dve območji primerni za invazijo.

Slika 2: Zemljevid potencialnih habitatov robinije na nižinskem testnem območju.

Glej angleški del prispevka.

NMRV se je dobro ujemala z dejansko prisotnostjo vrste na obeh testnih območjih (sliki 2 in 3). Obsežna območja dejanske prisotnosti vrste spadajo v napovedani razred z verjetnostjo nad 0,50. Nekatera druga območja dejanske prisotnosti, ki so bila izven tega razreda verjetnosti, smo vključili v naslednji razred (0,30–0,50), nekaj pa tudi v ostale razrede.

Slika 3: Zemljevid potencialnih habitatov robinije na testnem območju aluvialne ravnice reke Mure.

Glej angleški del prispevka.

Preglednica 1: Matrika za nižinsko testno območje ob pretvorbi v maksimalni TSS. Razvrstitev dejanskih in napovedanih prisotnosti/odsotnosti [1/0] robinije.

		dejanska prisotnost robinije	
		0	1
napovedana prisotnost robinije	0	25128	434
	1	4201	1368

Preglednica 2: Matrika za testno območje aluvialne ravnice reke Mure ob pretvorbi v maksimalni TSS. Razvrstitev dejanskih in napovedanih prisotnosti/odsotnosti [1/0] robinije.

		dejanska prisotnost robinije	
		0	1
napovedana prisotnost robinije	0	14301	230
	1	12160	2330

Rezultati matrike razvrstitev kažejo, da se je večina napovedanih prisotnosti ujemala z dejanskimi (preglednici 1 in 2). Kljub temu je iz preglednic razvidno, da so bili rezultati boljši na testnem območju aluvialne ravnice reke Mure.

Slika 4: Merjenje TPR za določitev napovedne točnosti na testnih območjih.

Glej angleški del prispevka.

Slika 5: Merjenje TSS za določitev napovedne točnosti na testnih območjih.

Glej angleški del prispevka.

Vrednosti TPR in TSS na izbranih prelomnih točkah na obeh testnih območjih so predstavljene na slikah 4 in 5.

Preglednica 3: Primerjava krivulj TPR z analizo variance parnih vzorcev in Tukeyjevim post hoc preizkusom.

	cena	st. napaka	z-vrednost	pomembnost
Mura: nižina = 0	0,007	0,003	2,353	$p < 0,1$
učno območje: nižina = 0	–0,011	0,003	–3,408	$p < 0,01$
učno območje: nura = 0	–0,018	0,003	–5,761	$p < 0,001$

Primerjava napovedi za učno območje in napovedi za testni območji razkrije pomembne razlike: napovedi za testni območji so bile slabše od tistih za učno območje (preglednica 3).

Z modelom razširjenosti vrste, ki smo ga oblikovali na učnem območju, smo uspešno izdelali zemljevide potencialne razširjenosti na testnih območjih. Kot pričakovano pa model dosega boljše napovedne rezultate na učnem območju kot na testnih območjih.

4 Razprava

Model razširjenosti robinije, ki ga je razvila Ribeiro s sodelavci (2011), smo uspešno prenesli na testni območji v isti geografski regiji. GLM se je izkazal za zanesljivo metodo modeliranja potencialnih habitatov vrste na novih območjih; rezultat se ujema z ugotovitvijo Randina s sodelavci (2006), da je GLM zanesljiva metoda modeliranja prenosljivosti. V nasprotju s tem je Araújo s sodelavci (2005) ugotovil, da je generalizirani aditivni model (GAM) bolje prenosljiv kot GLM.

Na splošno je NMRV zadovoljivo napovedal potencialno razširjenost robinije v Prekmurju, vendar pa so se pomembne razlike pokazale glede njegove uspešnosti na obeh testnih območjih. Kljub temu lahko zaključimo, da se model lahko zadovoljivo uporablja tudi na malce drugačnem geografskem območju, četudi znotraj iste regije.

V večini raziskav, v katerih so raziskovalci modele preskušali zunaj učnega območja, je uporabljeno samo eno testno območje (npr. Randin s sod. 2006; Fukasawa s sod. 2009; Sundblad s sod. 2009; Preuss s sod. 2011); raziskav, v katerih je bilo uporabljeno več kot eno testno območje, pa je zelo malo (Zimmermann in Kienast 1999; Wenger in Olden 2012). Naša raziskava tako pomembno prispeva k zbirki tovrstnih raziskav. Kljub temu jo lahko na druge geografske regije posplošimo le do določene mere, pa tudi pri prenosu njenih rezultatov moramo biti previdni; skrbno moramo namreč preučiti osnovne okoljske napovedne dejavnike (prediktorje). Eden najpomembnejših pogojev praktične uporabe modelov razširjenosti vrst, na podlagi katerih lahko sprejemamo odločitve s področja upravljanja okolja, je njihova prenosljivost znotraj iste regije in med različnimi regijami. Kot je ugotovil Barbosa s sodelavci (2009), ti modeli najboljše opišejo prostorski vzorec razširjenosti vrste na območju, na katerem je bil model razvit, in sicer predvsem zato, ker lahko med različnimi območji obstajajo razlike v obsegu okoljskih napovednih dejavnikov (Randin s sod. 2006). Okoljske razlike med različnimi geografskimi regijami lahko zato omejujejo uporabnost tovrstnih modelov, poleg tega pa lahko ti modeli dajejo nerealne napovedi zunaj območja, na katerem so bili prvotno razviti (Barbosa s sod. 2009). Razpoložljivost podatkov je lahko pri prostorskem prenosu teh modelov omejitveni dejavnik. Poleg te omejitve na prenosljivost na druga območja vplivajo tudi izbire med samim postopkom modeliranja, kot je recimo izbira tehnike modeliranja; to sta potrdila tudi Araújo s sodelavci (2005) ter Randin s sodelavci (2006). Ocena zanesljivosti tehnik modeliranja pri prenosu modela z ene geografske regije na drugo je presejala okvire naše raziskave; uspelo pa nam je model prenesti znotraj iste geografske regije.

Največja vrednost raziskave leži v dejstvu, da lahko napovedi verjetnosti pojava obravnavane vrste na neraziskanih območjih upravljalce opozorijo na morebitne nevarnosti zasaditve te vrste oziroma njenega spontanega razraščanja, kar jim lahko pomaga pri načrtovanju zaščitnih ukrepov. Pokazali smo, da lahko napovedni model, ki smo ga testirali v tej raziskavi, zanesljivo uporabimo za oblikovanje napovedi znotraj iste regije in osveščanje javnosti o tej invazivni rastlinski vrsti. To je ključnega pomena za preprečevanje njene nadaljnje širitve, še zlasti na obravnavanem območju, kjer domačini večinoma še vedno zaznavajo zgolj njene koristi. Že izdelani model napovedi morebitnega obsega razširitve robinije je preprosto orodje, s katerim lahko upravljalci omilijo posledice te invazivne rastlinske vrste, in rešitev, ki je učinkovitejša od dolgotrajnega in logistično zahtevnega postopka zbiranja podatkov.

5 Literatura

Glej angleški del prispevka.

